

PROTEIN	DESCRIPTION	REFERENCE <sup>1</sup>	mRNA/gene Sequence <sup>2</sup>
VOLTAGE-GATED ION CHANNEL	K+ CHANNEL BETA 1A SUBUNIT	Hs.45090	U33428 L39833 L47665
SODIUM CHANNEL	VOLTAGE DEPENDANT SODIUM CHANNEL		
CALCIUM CHANNEL	DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-1-B1 SUBUNIT	Hs.635	L0611 M92392 M76560
	DIHYDROPYRIDINE-SENSITIVE L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (CACNLIA3),	Hs.1294	L33798 U30707
	NEURONAL DHP-SENSITIVE, VOLTAGE-DEPENDENT, CALCIUM CHANNEL ALPHA-2b SUBUNIT	Hs.1295	M76559
	DIHYDROPYRIDINE-SENSITIVE 1-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT	Hs.1296	L07738 Z19603
	NEURONAL DHP-SENSITIVE, VOLTAGE-DEPENDENT, CALCIUM CHANNEL ALPHA-1D SUBUNIT	Hs.23838	M76558 M83556 D43747
	PUTATIVE CALCIUM INFLUX CHANNEL (htrp3)	H.24852	U47050 Y13758
	VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-1 E-3	Hs.65441	L29385 L29384 L27745
	N-TYPE CALCIUM CHANNEL ALPHA- SUBUNIT	Hs.69949	M94172 M94173
	VOLTAGE-DEPENDENT L-TYPE Ca CHANNEL ALPHA 1 SUBUNIT	Hs.89925	L29536 L29534 M92269

<sup>1</sup> GENBANK REFERENCE DESIGNATION FOR PROTEIN. PROTEINS WITH NO DESIGNATION ARE REFERENCED IN THIS TEXT.

<sup>2</sup> GENBANK mRNA OR GENE SEQUENCE REFERENCE DESIGNATION.

FIG. 1-A

2/27

PROTEIN	DESCRIPTION	REFERENCE	mRNA/gene Sequence
LIGAND-GATED CHANNEL	GAMMA-AMINO BUTYRIC ACID (GABA) RECEPTOR NICTOTINIC ACETYLCHOLINE RECEPTOR		
G-COUPLED RECEPTOR	P2Y6 RECEPTOR	Hs.16362	AF007891 U52464
	CHEMOKINE (C-C) RECEPTOR 7	Hs.784	L08177
	HUMAN RPE-RETINAL G PROTEIN-COUPLED RECEPTOR	Hs.1544	U14910
	INWARDLY RECTIFYING POTASSIUM CHANNEL KIR3.2	Hs.11173	U52153 D87327 U24660
	G PROTEIN-COUPLED RECEPTOR KINASE GRK4	Hs.32859	L03718 U33054
	G PROTEIN-COUPLED INWARDLY RECTIFYING POTASSIUM CHANNEL Kir3.4	Hs.37168	U52154
	G PROTEIN-ACTIVATED INWARDLY RECTIFYING POTASSIUM CHANNEL HGIRK1/Kir3.1	Hs.37169	U50964
RECEPTOR-GATED CHANNEL	Fc FRAGMENT OF IgE, HIGH AFFINITY 1, RECEPTOR FOR: BETA POLYPEPTIDE	Hs.30	M89796
	INTERLEUKIN 2 RECEPTOR GAMMA CHAIN	Hs.84	L19546
	CHOLECYSTOKININ A RECEPTOR	Hs.129	L13605 L19315
	PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR	Hs.202	M36035
	CHOLECYSTOKININ B RECEPTOR	Hs.203	L07746 L10822
	GLUCAGON RECEPTOR	Hs.208	L20316
	SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR	Hs.220	L11695
	FORMYL PEPTIDE RECEPTOR-LIKE 1	Hs.251	M84562 M88107
	ADENOSINE RECEPTOR A3	Hs.258	L20463 L22607

FIG. 1-B

PROTEIN	DESCRIPTION	REFERENCE	mRNA/gene Sequence
GROWTH FACTOR RECEPTOR	PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1)	Hs.44	M57399
	HEPATOCYTE GROWTH FACTOR ACTIVATOR RECURSOR	Hs.104	D14012
	FIBROBLAST GROWTH FACTOR 9 (GLIA-ACTIVATING FACTOR)	Hs.111	D14838
	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2	Hs.162	M35410
KINASE	HUMAN GROWTH FACTOR RECEPTOR TYROSINE KINASE (STK-1)	Hs. 385	U02687
	PROTO-ONCOGENE C-COT (PROTEIN-SERINE/THREONINE KINASE)	Hs.248	D14497
	RECEPTOR PROTEIN-TYROSINE KINASE SKY	Hs.301	U18934 D17517
	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IV	Hs.348	D30742 L24959
	CREATINE KINASE B	Hs.669	M16451 L47647
TRANSFERASE	V-raf MURINE SARCOMA VIRAL ONCOGENE HOMOLOG B1	Hs.662	M95712
	GLUCOSAMINYL (N-acetyl) TRANSFERASE 1, CORE 2	Hs.781	M97347 L41415
	GLUTATHIONE S-TRANSFERASE, MICROSOMAL	Hs.790	J03746
	UDP GLUCOSYLTRANSFERASE 8 (UDP-GALACTOSE CERAMIDE GALACTOSYLTRANSFERASE)	Hs.57700	U30930 U62899
ISOMERASE	PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B)	Hs.699	
	3-BETA HYDROXY-5-ENE STEROID DEHYDROGENASE TYPE II	Hs.825	M67466 N77144
	GLUCOSE PHOSPHATE ISOMERASE	Hs.944	K03515
	HYDROXY-DELTA-5-STEROID DEHYDROGENASE, 3-BETA- AND STEROID DELTA-ISOMERASE 1	Hs.38586	M27137 M38180
PROTEASE	26S PROTEASE REGULATORY SUBUNIT 4	Hs.548	L02426
	HEPSIN	Hs.823	M18930
	GRANZYME B PRECURSOR	Hs.1051	M17016
DEHYDROGENASE	GLYCINE CLEAVAGE SYSTEM PROTEIN P (GLYCINE DECARBOXYLASE)	Hs.27	M64590
	17 BETA HYDROXYSTEROID DEHYDROGENASE, TYPE 2	Hs.181	L11708

FIG. 1-C

PROTEIN	DESCRIPTION	REFERENCE	mRNA/gene Sequence
DEHYDROGENASE	XANTHINE DEHYDROGENASE	Hs.250	D11456
	ALCOHOL DEHYDROGENASE 7 SIGMA SUBUNIT (CLASS IV)	Hs.389	U09623 U07821
	SUCCINATE DEHYDROGENASE 2, FLAVOPROTEIN (Fp) SUBUNIT	Hs.469	D30648 L21936
SYTHETASE	LONG CHAIN FATTY ACID ACYL-coA LIGASE	Hs.34	L09229
	FOLYL POLYGLUTAMATE SYNTHETASE	Hs.754	M98045
	GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC	Hs.1673	M90656
DEAMINASE	HYDROXYMETHYLBILANE SYNTHASE	Hs.82609	M95623
	DIPEPTIDYLPEPTIDASE IV (CD26, ADENOSINE DEAMINASE COMPLEXING PROTEIN 2)	Hs.44926	M80536
	DEOXYCYTIDYLATE DEAMINASE	Hs.76894	L12136
ONCOGENE	AMP DEAMINASE 2	Hs.82927	U16270
	ADENOSINE MONOPHOSPHATE DEAMINASE (ISOFORM E)	Hs.83918	M84721
	V-erb AVIAN SARCOMA VIRUS CT10 ONCOGENE HOMOLOG	Hs.16	D10656
	THYROID HORMONE RECEPTOR, ALPHA (AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL (v-erb-a) ONCOGENE HOMOLOG)	Hs.724	M24899
	FRIEND LEUKEMIA VIRUS INTEGRATION I	Hs.736	M98833
	RAP1A, MEMBER OF RAS ONCOGENE FAMILY	Hs.865	M22995
	THROMBOPOIETIN (MYELOPROLIFERATIVE LEUKEMIA VIRUS ONCOGENE LIGAND, MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR	Hs.1166	L36051
	FIBROBLAST GROWTH FACTOR 4 (HEPARIN SECRETORY TRANSFORMING PROTEIN 1, KAPOSI SARCOMA ONCOGENE)	Hs.1755	J02986 M17446
	V-erb-a AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG-LIKE 4	Hs.1939	L07868
FOS	P55-c-fos PROTO-ONCOGENE PROTEIN	Hs.25647	V01512
JUN	C-jun PROTO ONCOGENE (JUN)	Hs.78465	J04111
	Jun B PROTO-ONCOGENE	Hs.89792	M29039

FIG. 1-D





6/27

CANINE LV MYOCYTES INFECTED  
WITH dGFP or AdHERG

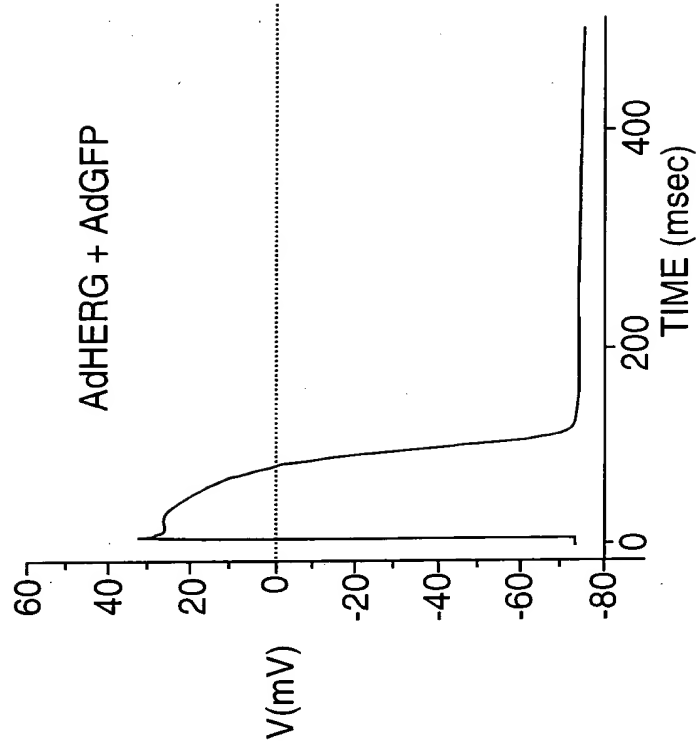


FIG. 2B

CANINE LV MYOCYTES INFECTED  
WITH dGFP or AdHERG

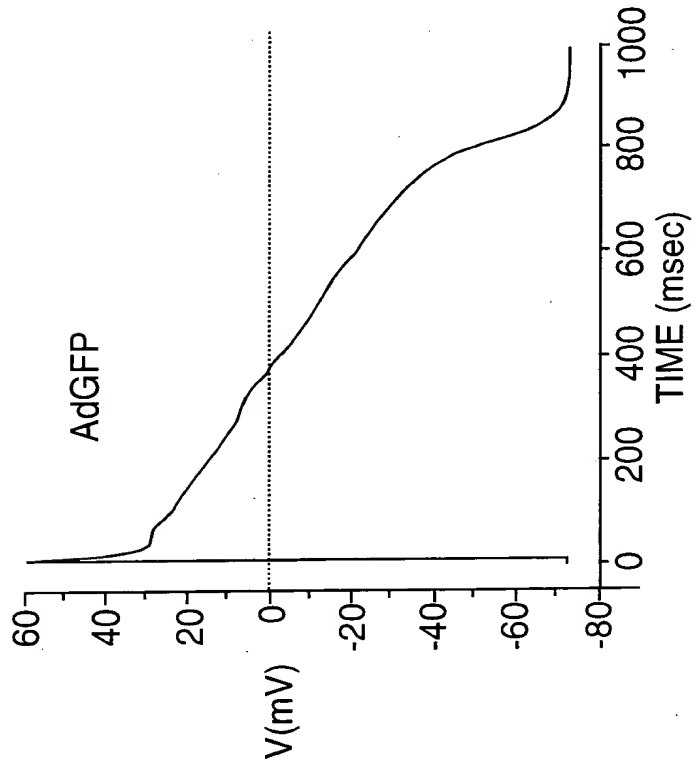
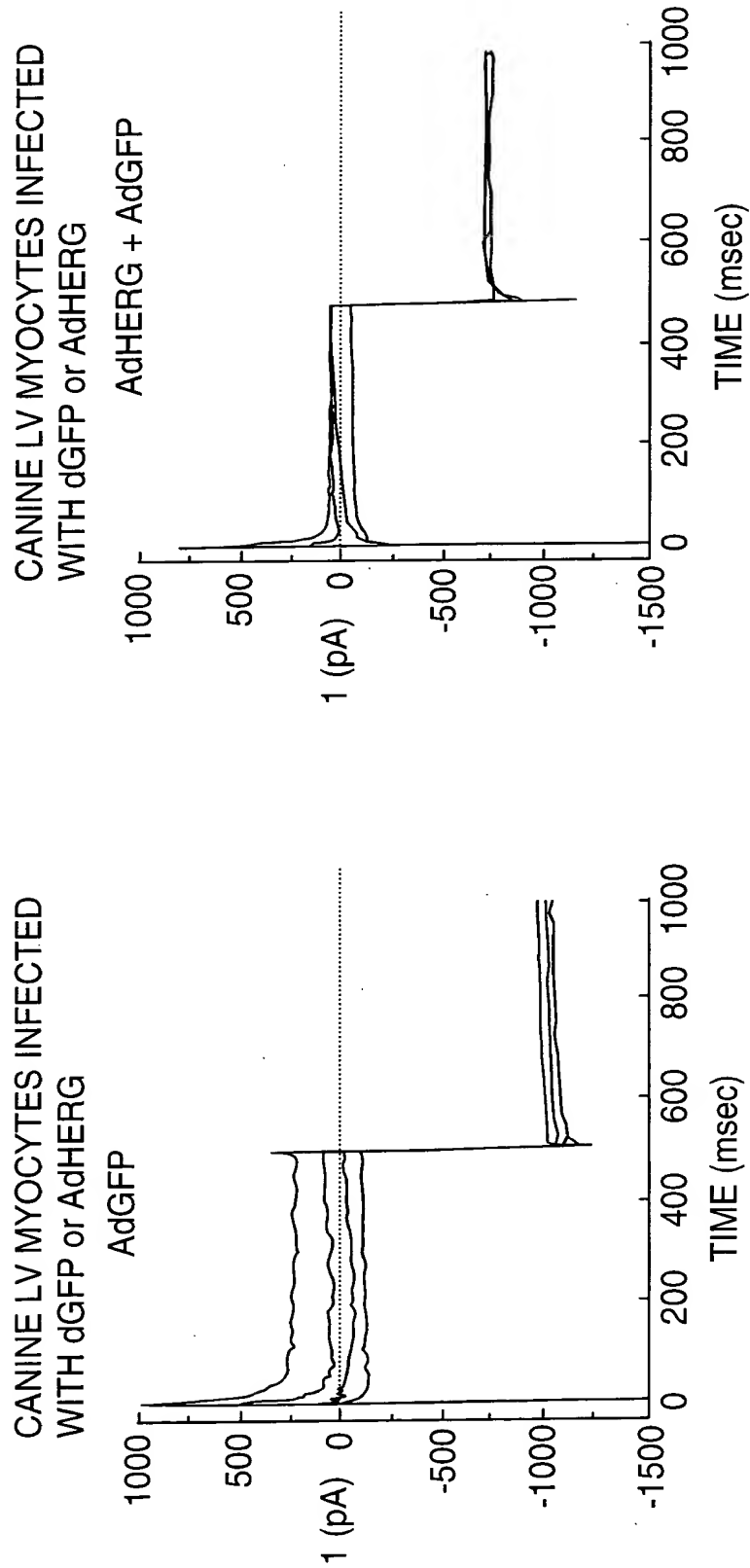


FIG. 2A

7/27



8/27

CANINE LV MYOCYTES INFECTED  
WITH dGFP or AdHERG

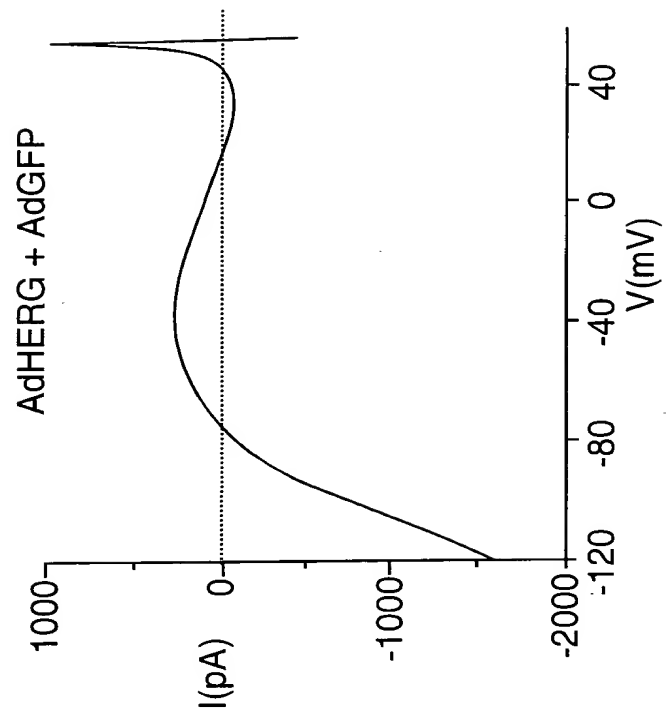


FIG. 2F

CANINE LV MYOCYTES INFECTED  
WITH dGFP or AdHERG

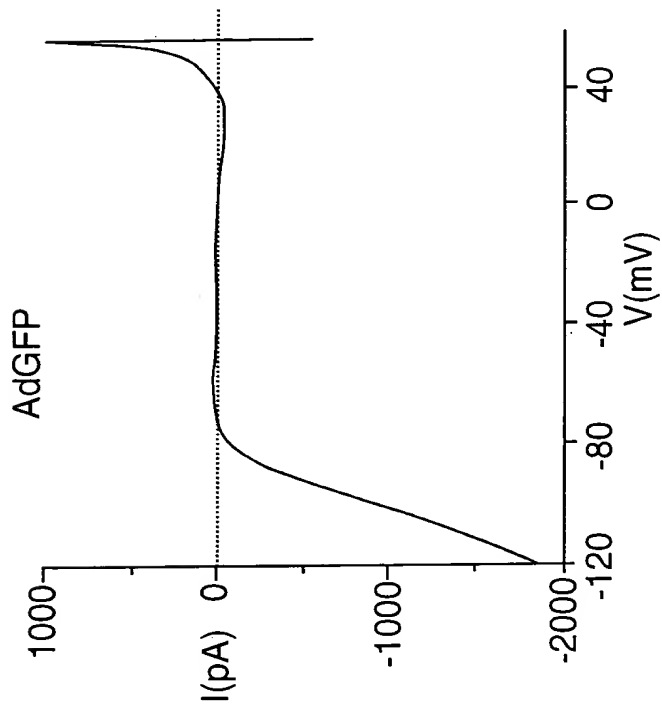


FIG. 2E



# SCHEMATIC

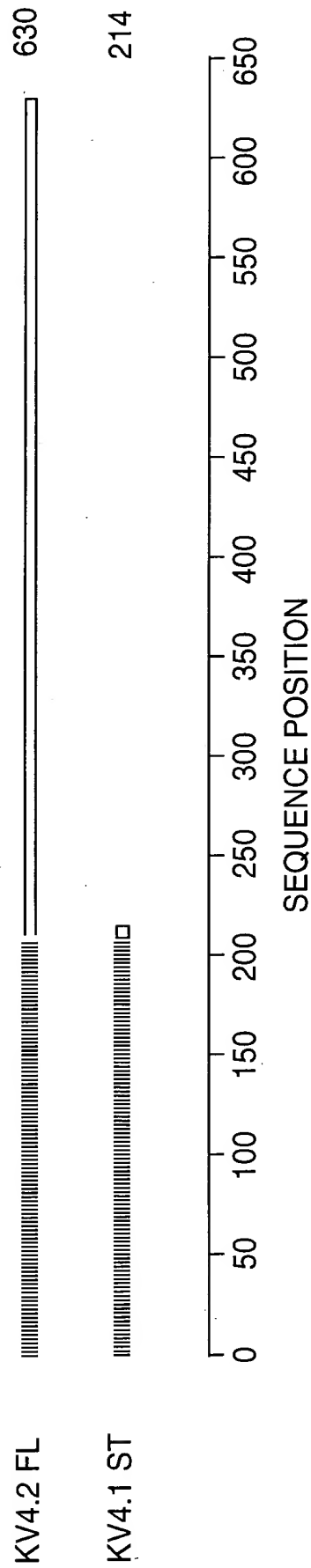


FIG. 3A

10/27

ALIGNMENT

KV4.2 FL KV4.2 ST	MAAGVAAWLPEFAAAAIGWMPVASGMPAPPQERKRTQDALIVLNVSGTRFQTWQDTLE MAAGVAAWLPEFAAAAIGWMPVASGMPAPPQERKRTQDALIVLNVSGTRFQTWQDTLE	60 60
KV4.2 FL KV4.2 ST	RYPDTLLGSSERDFFYHPETQQYFFDRDPDI FRHILNFYRTGKLHYPRHECISAYDEELA RYPDTLLGSSERDFFYHPETQQYFFDRDPDI FRHILNFYRTGKLHYPRHECISAYDEELA	120 120
KV4.2 FL KV4.2 ST	FEGLIPEIIGDCCYEEYKDRRRENAERLQDDADTDNTGESALPTMTARQVRWRAFENPHT FEGLIPEIIGDCCYEEYKDRRRENAERLQDDADTDNTGESALPTMTARQVRWRAFENPHT	180 180
KV4.2 FL KV4.2 ST	STMALVFYVVTGFFIAVSVIANVVEtVpcgsspgghikelpcgeryavaffcldtacvmif STMALVFYVVTGFFIAVSVIANVVEtVpcgsspgghikelpcgeryavaffcldtacvmif	240 214
KV4.2 FL KV4.2 ST	tveyllrlaapsryrfvsvmsiidvailpyyiglvmtdnedvsgafvtrvfrvfri -----	300 214
KV4.2 FL KV4.2 ST	fkfshrsgglrilgytlkscaselgllflsltmaliiifatvmfyaekgssaskftsipaa -----	360 214
KV4.2 FL KV4.2 ST	fwytivtmttlgygdmvpktiagkifgsicslsgvlvialpvpvsvnsfryhqnqgrad -----	420 214
KV4.2 FL KV4.2 ST	krraqkkarlariraaksgsanaymqskrngllsnqlqssedepafvsksgssfetqhhh -----	480 214
KV4.2 FL KV4.2 ST	llhclekttnhefvdeqvfeescmevatvnrpsshpslssqqgvtstccsrrhkktfri -----	540 214

FIG. 3B



KV4.2 FL  
KV4.2 ST

pnansgshrgsvqelstiqircvertplnsrsslakmeecvklncegpyvttaiisi  
-----

600  
214

KV4.2 FL  
KV4.2 ST

ptppvttpegddrpespeysggnivrval  
-----

630  
214

11/27

FIG. 3C

12/27

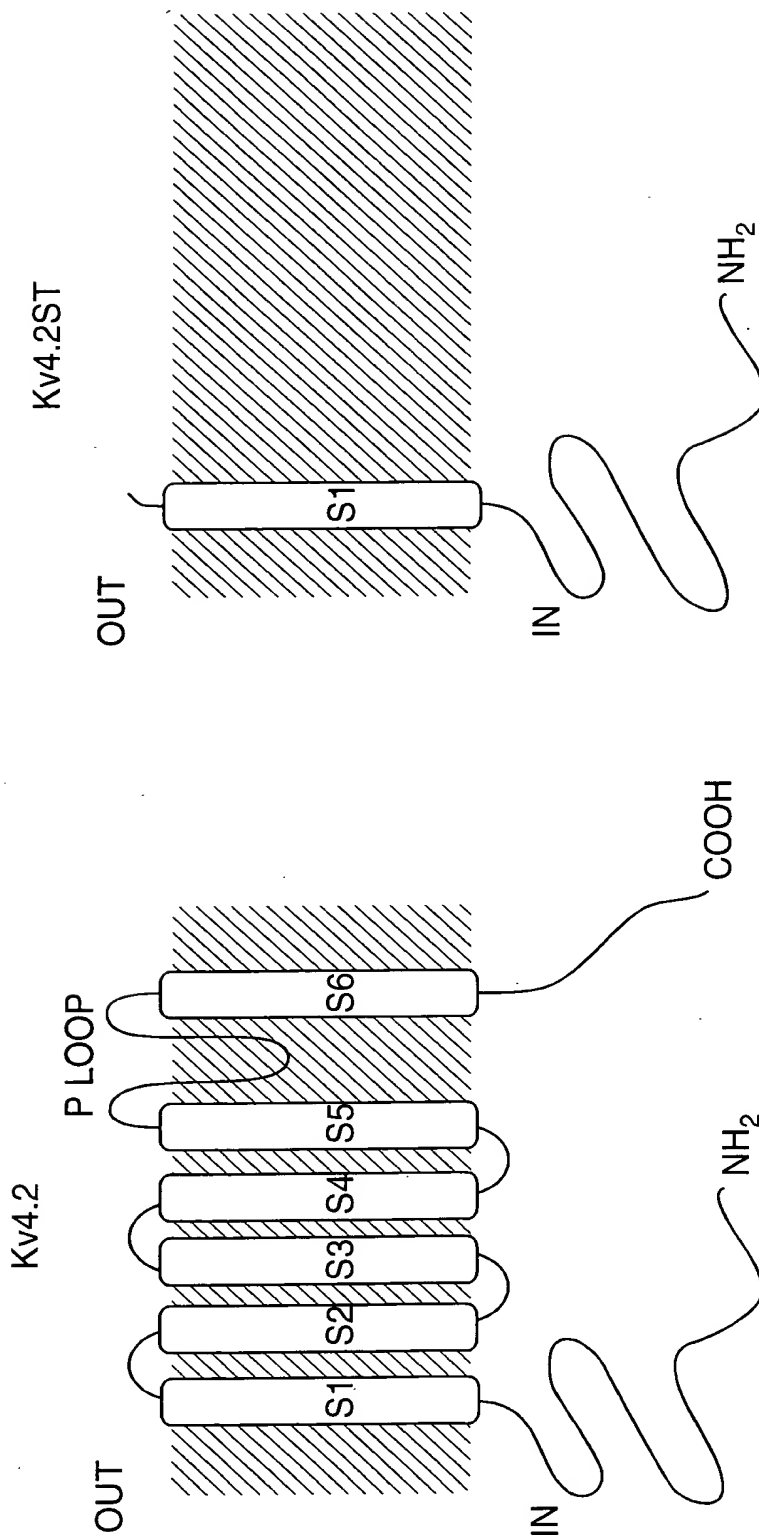


FIG. 4A

FIG. 4B

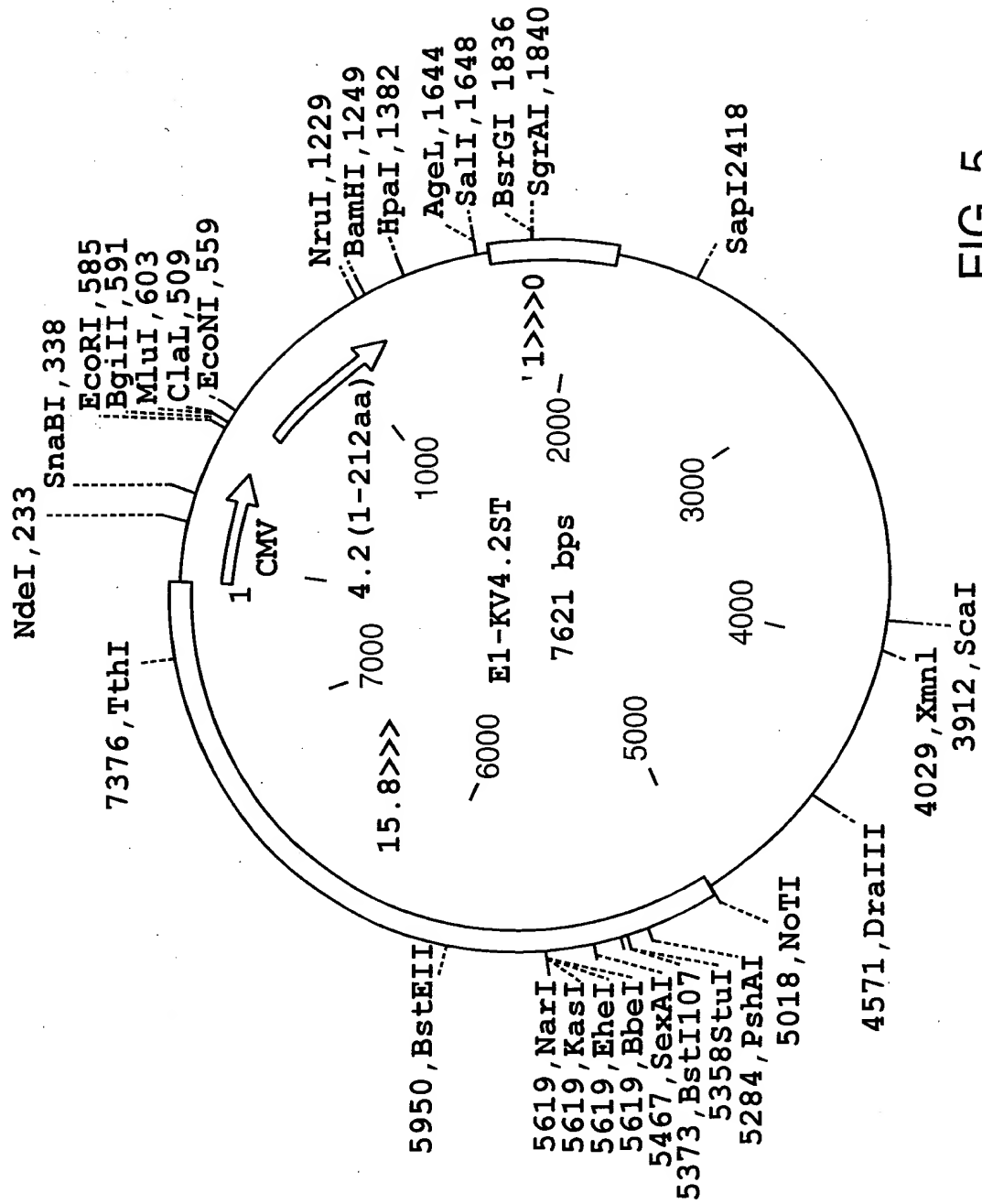


FIG. 5

14/27

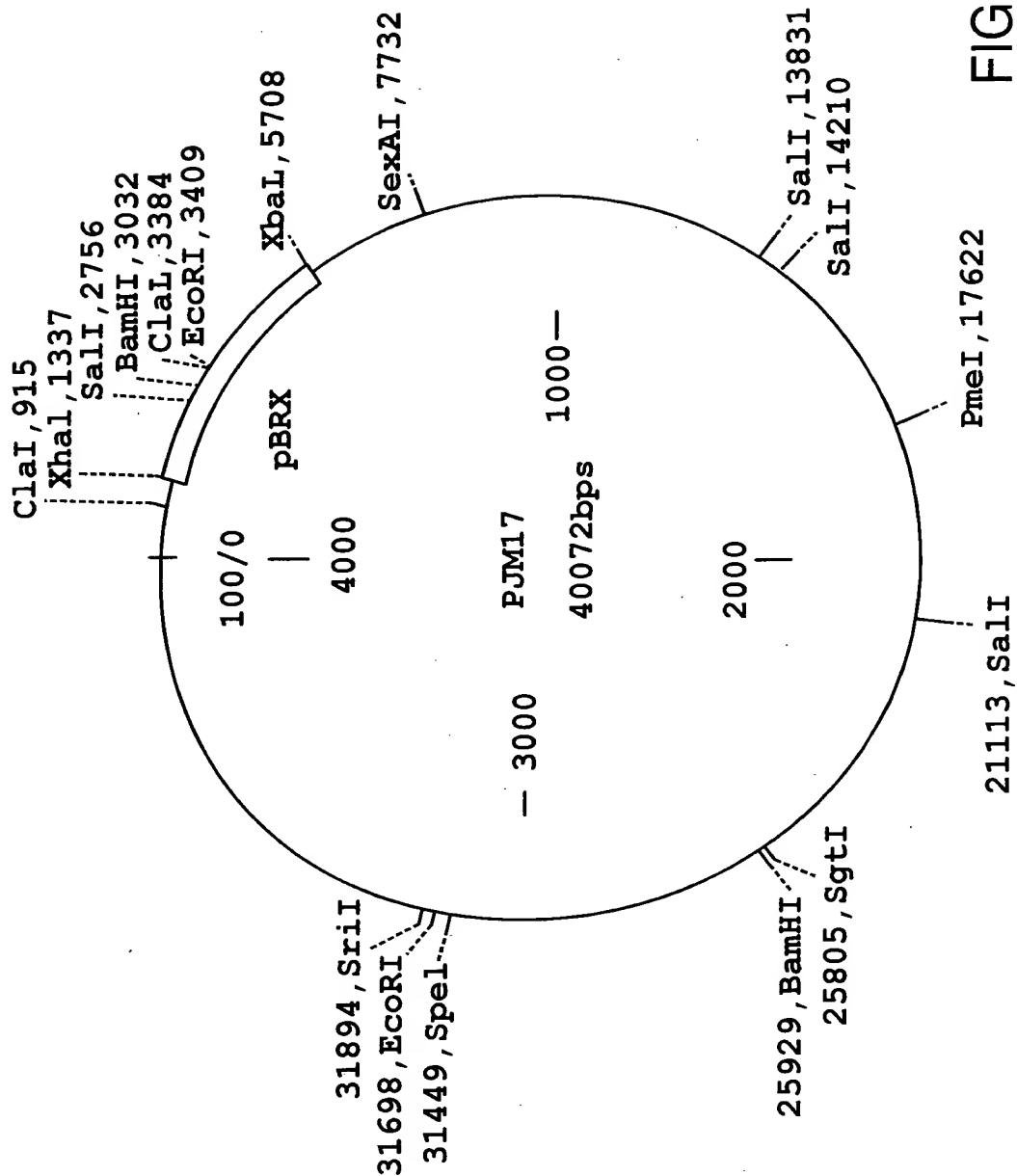
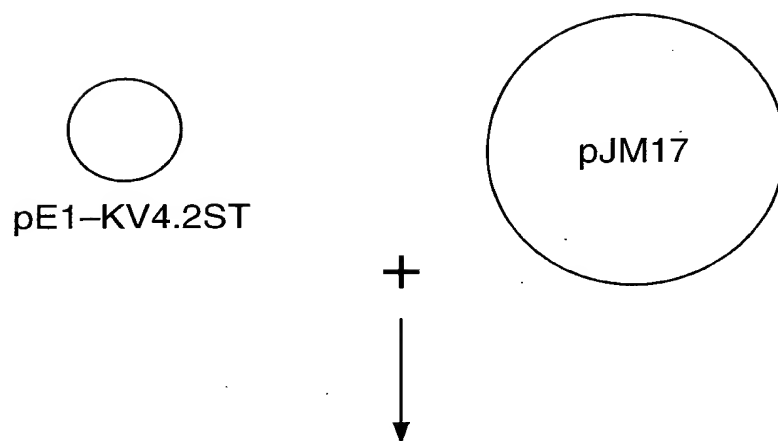


FIG. 6



15/27



AdKv4.2ST

FIG. 7A

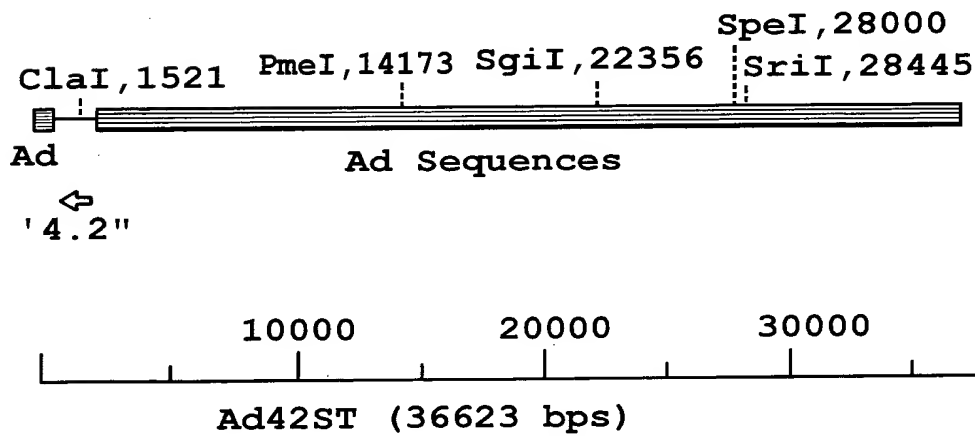


Fig.7B

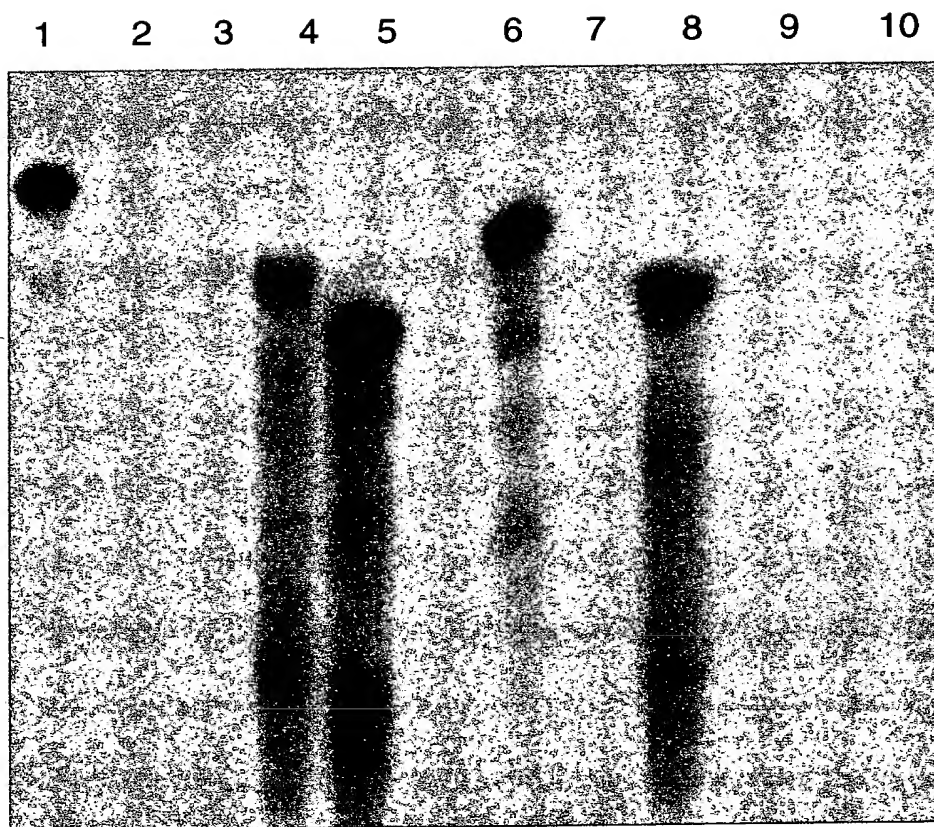


FIG. 8

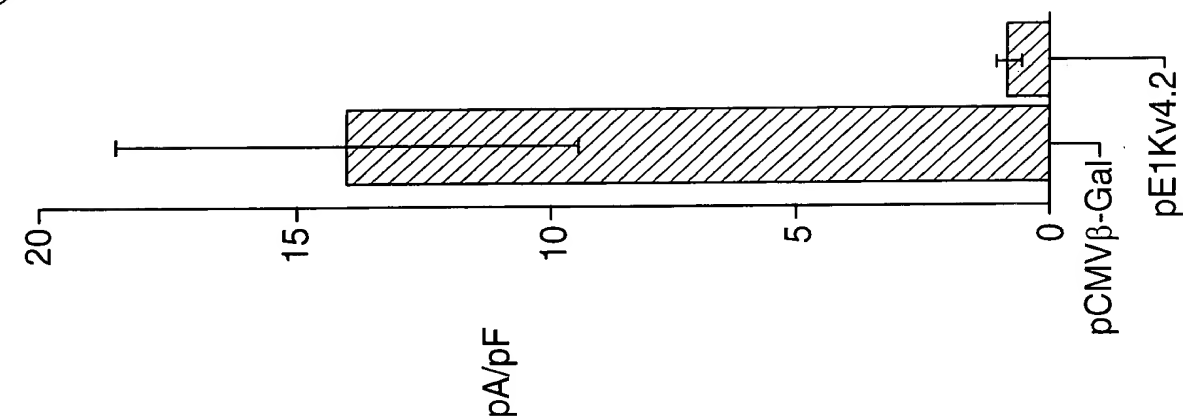


FIG. 9C

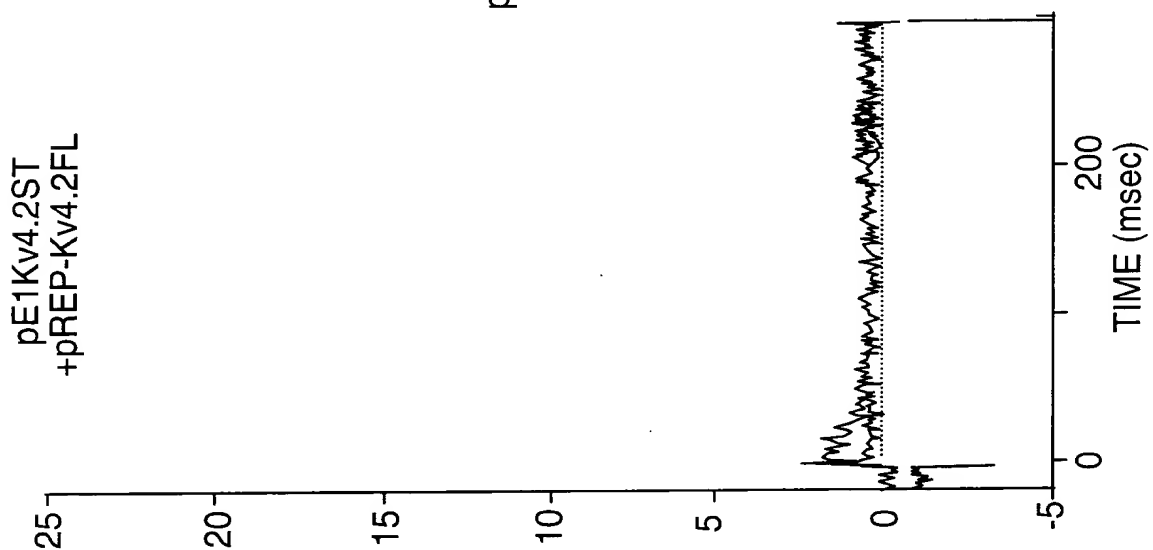


FIG. 9B

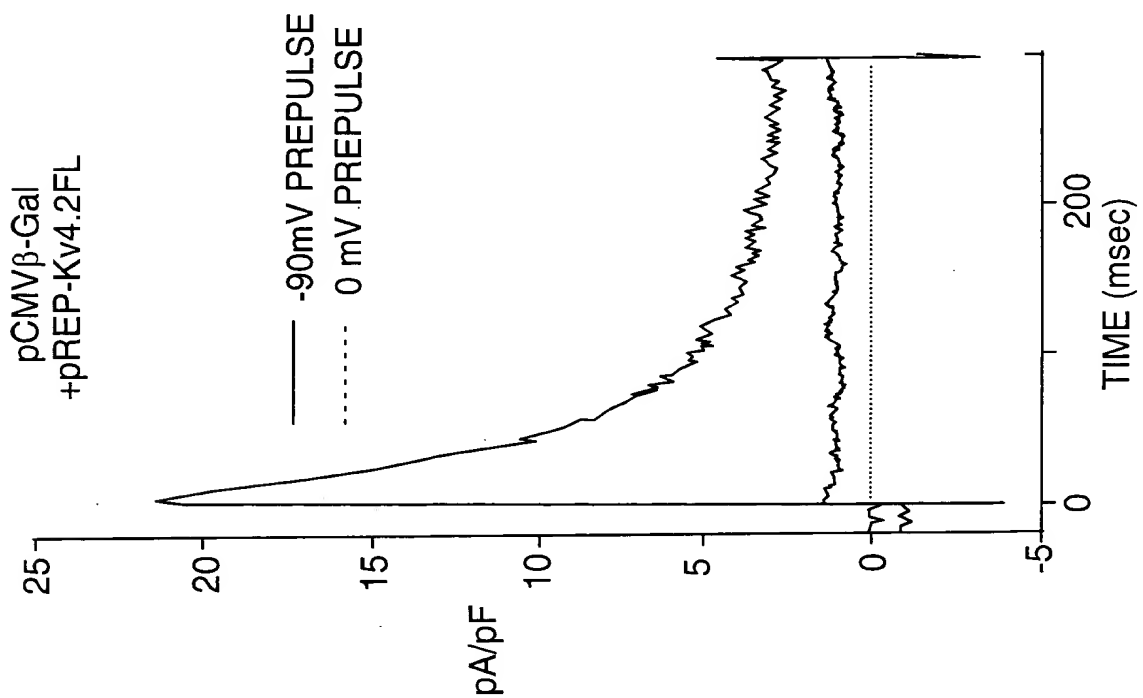


FIG. 9A

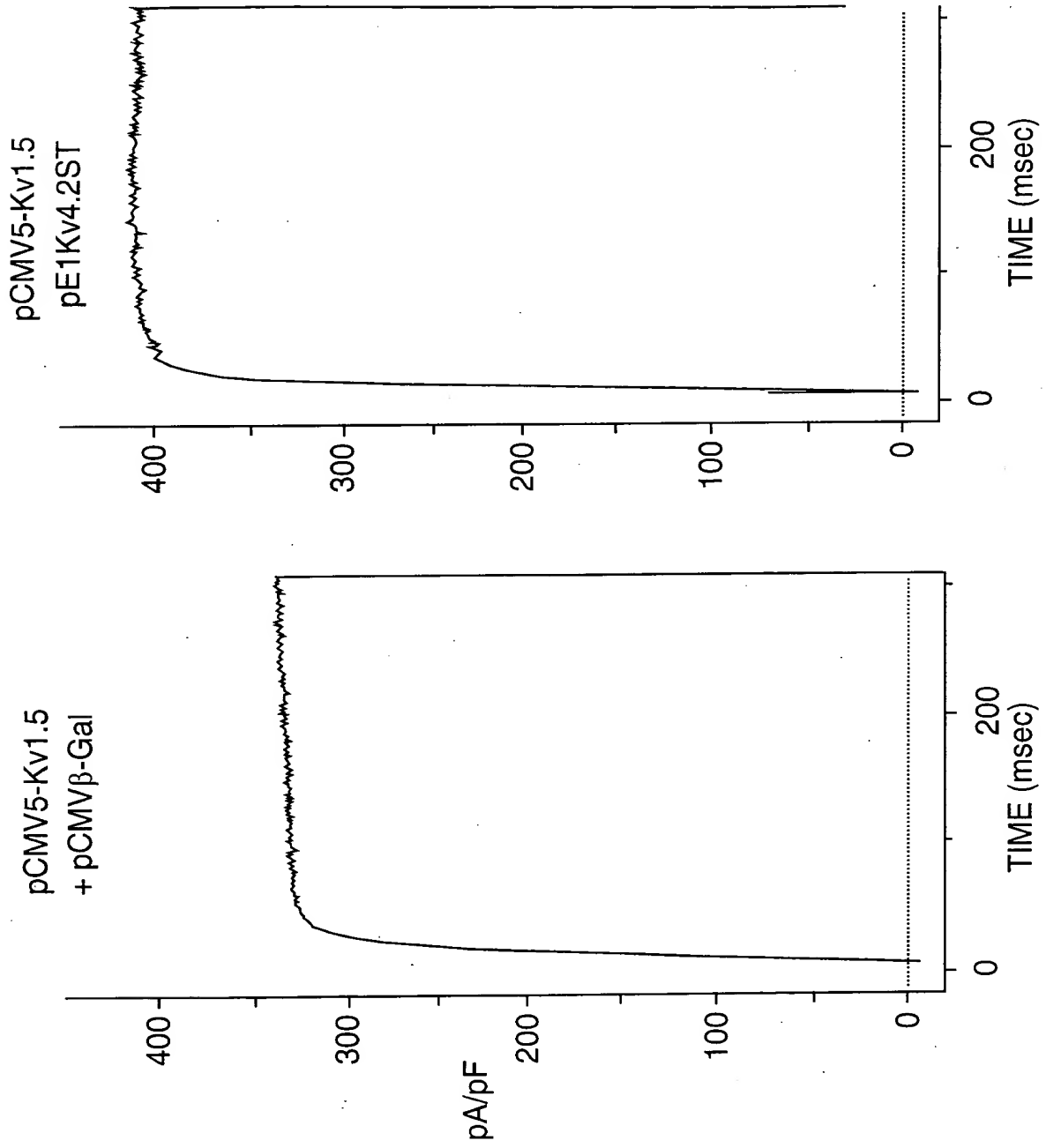


FIG. 9D

FIG. 9E

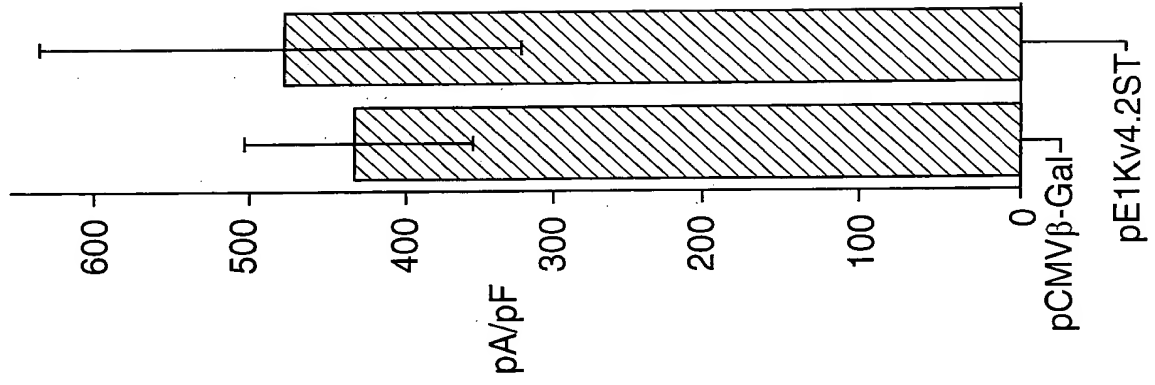
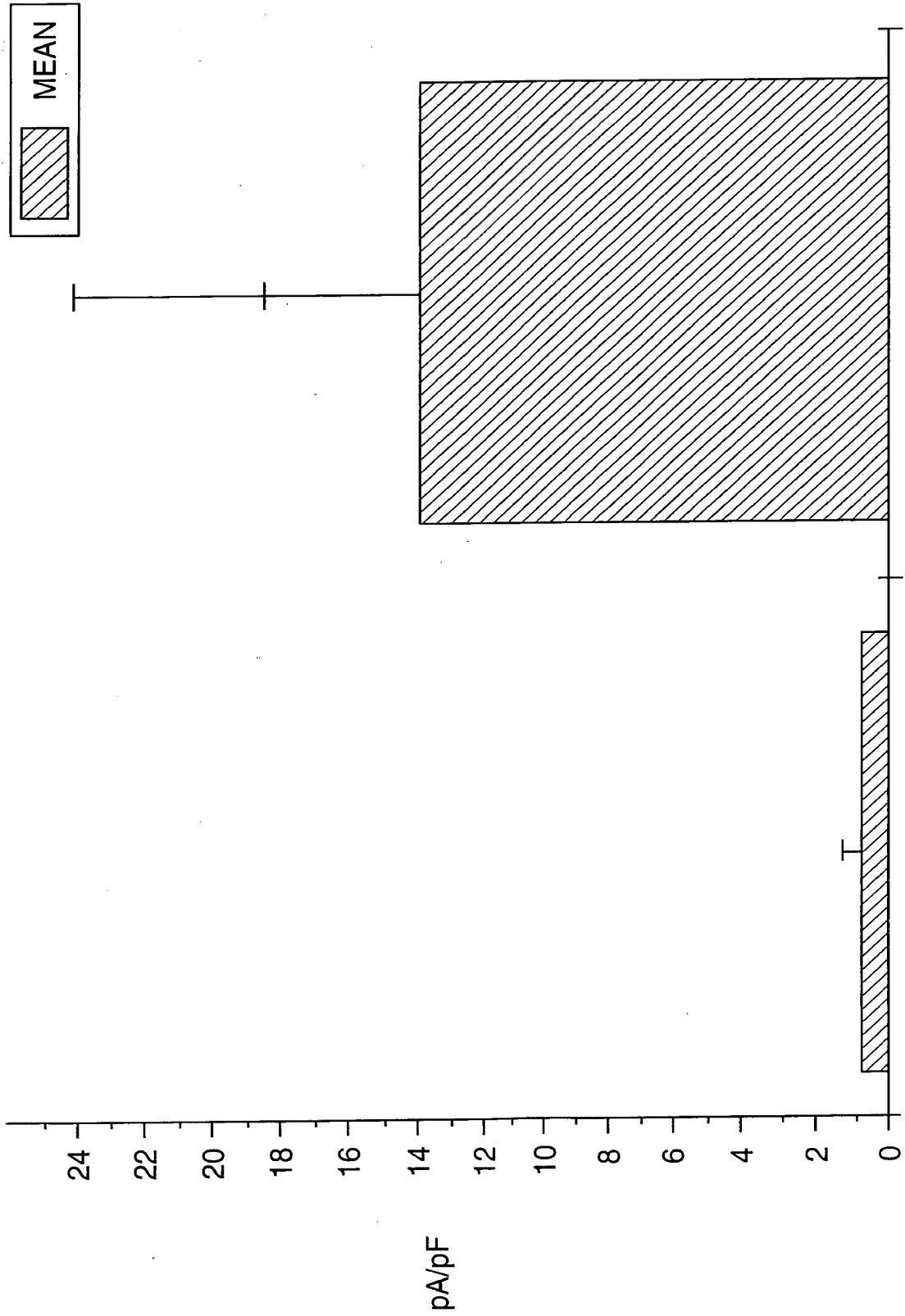


FIG. 9F

19/27



BETA GAL  
FIG. 10B

4.2ST  
FIG. 10A

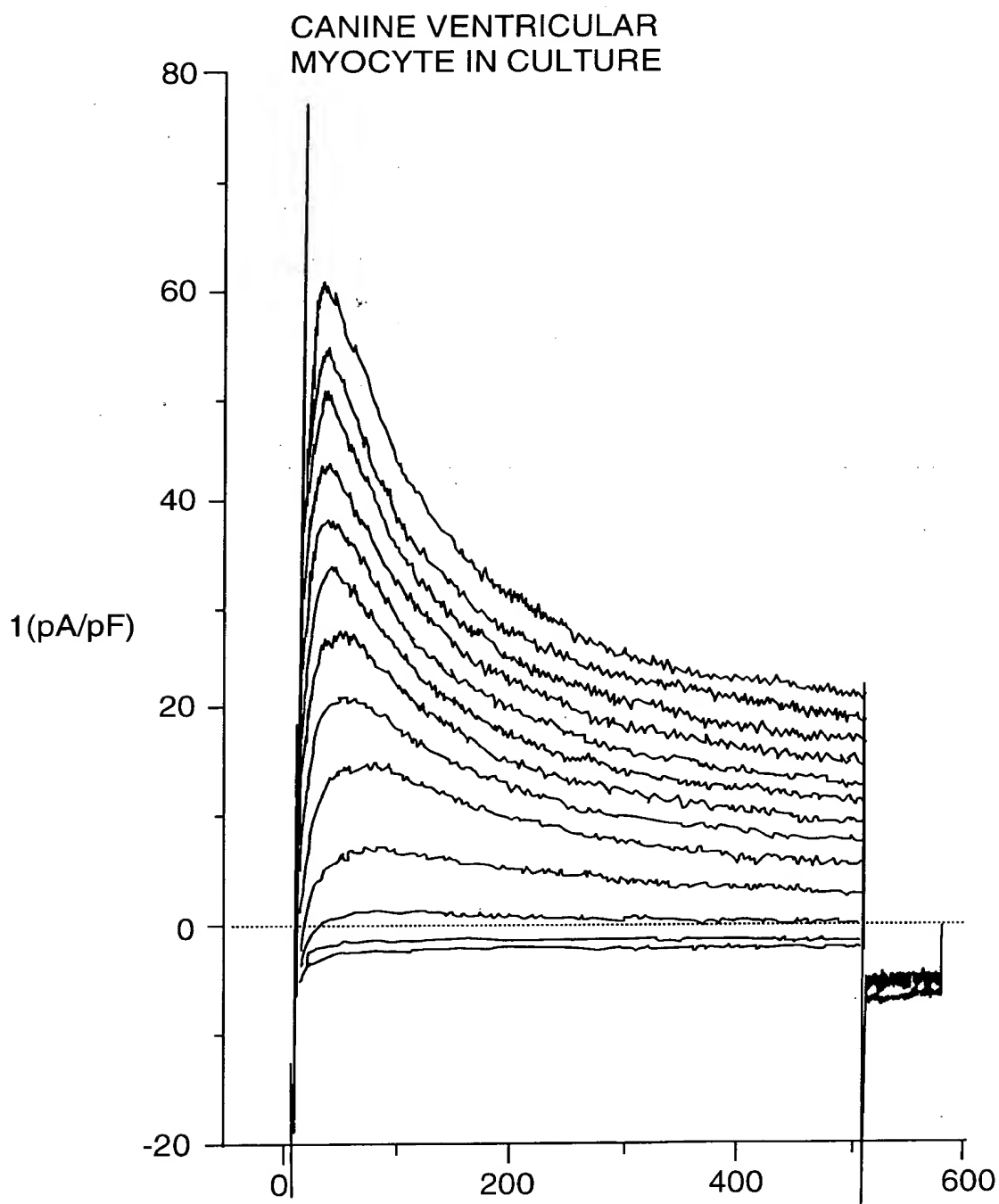


FIG. 11A

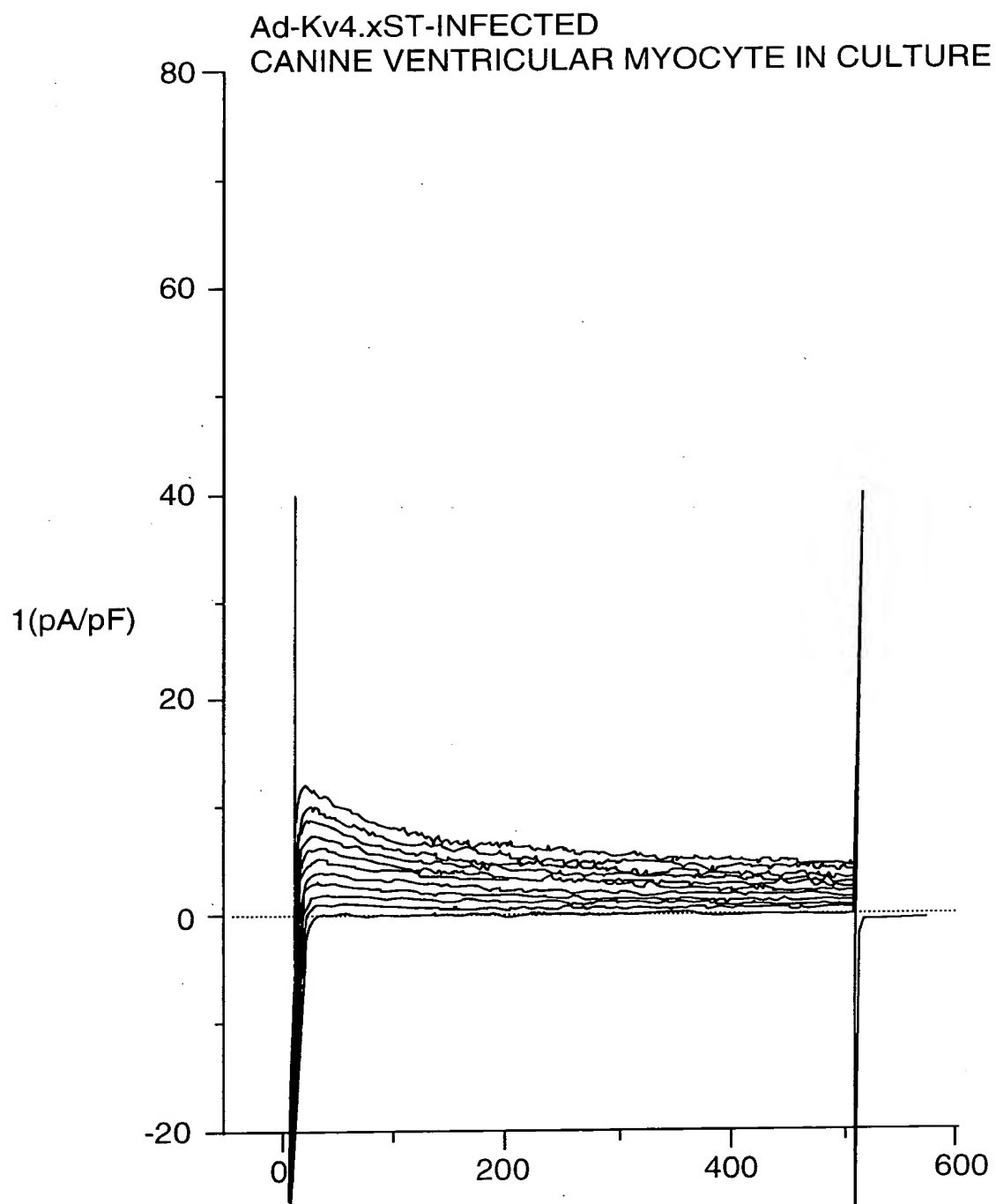


FIG. 11B

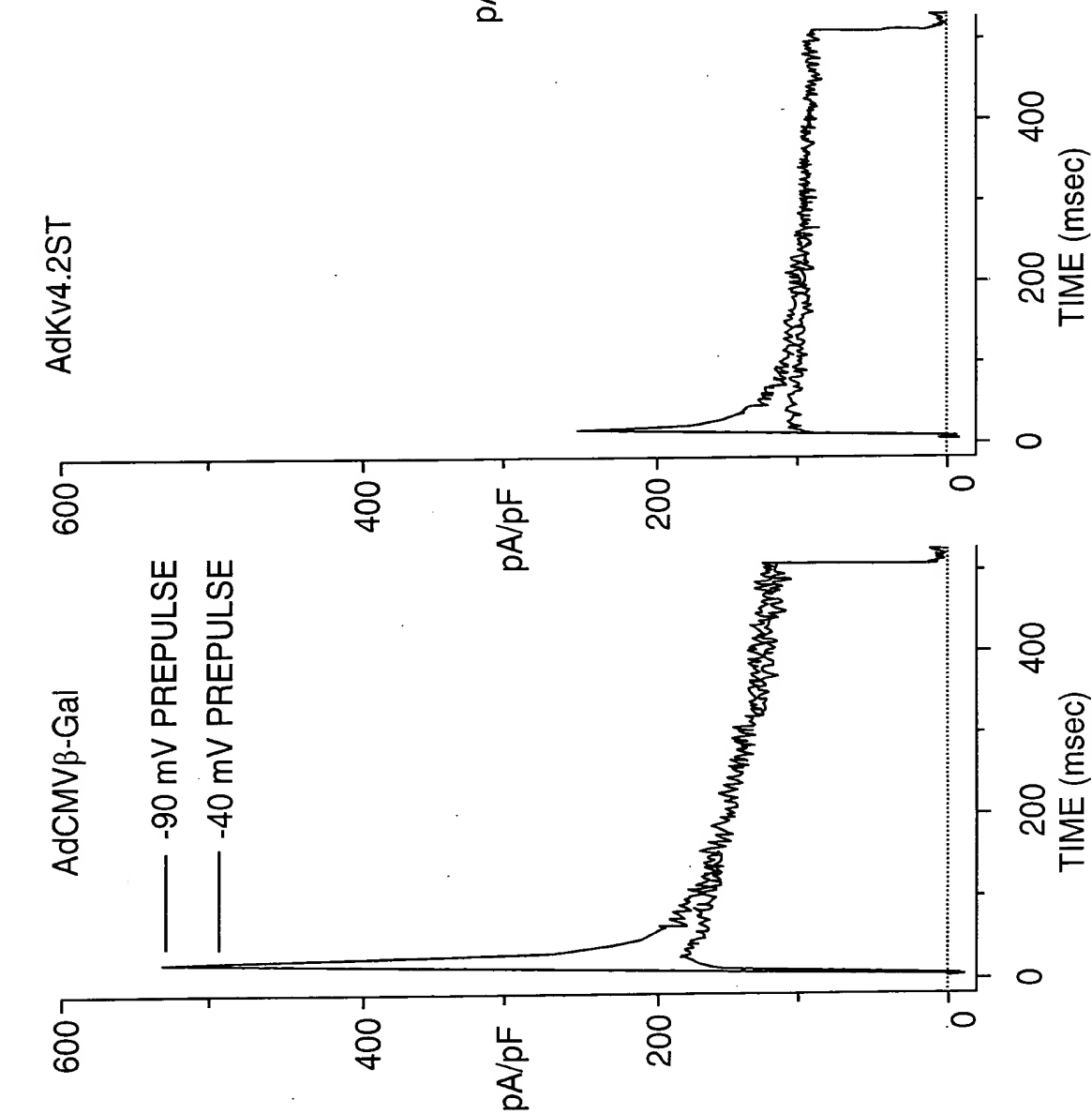


FIG. 12A

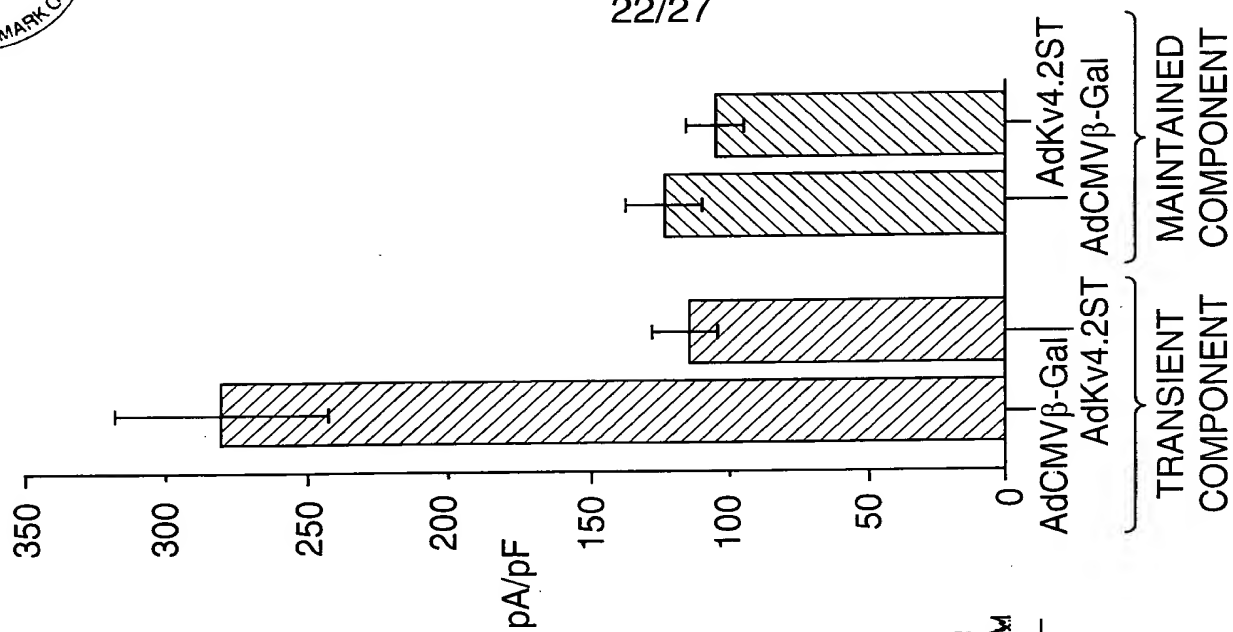


FIG. 12C

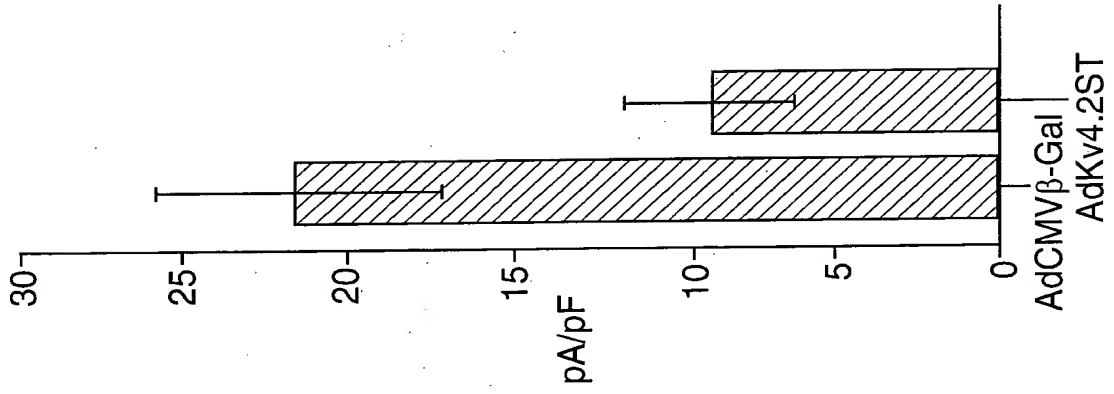


FIG. 13C

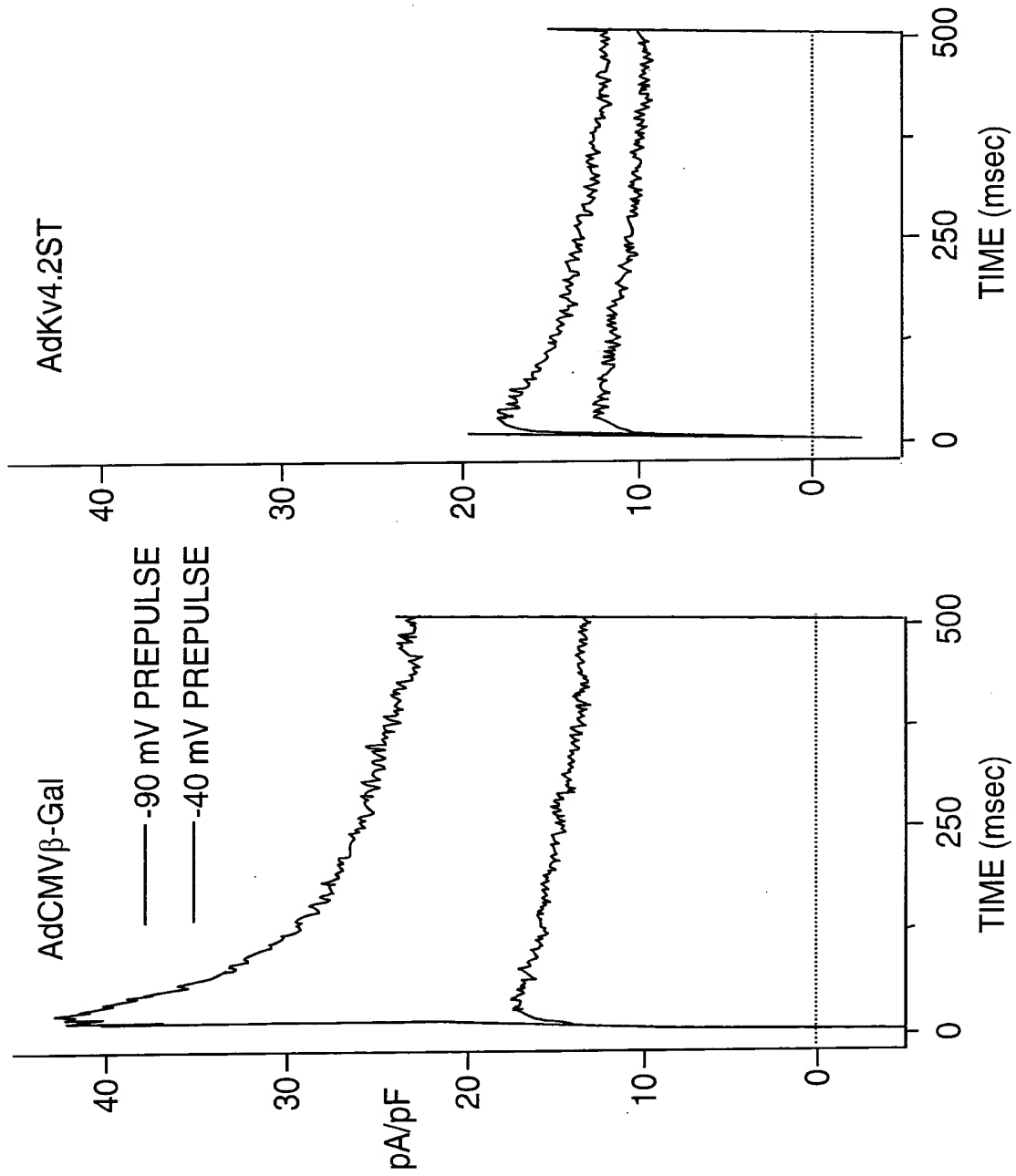


FIG. 13B

FIG. 13A

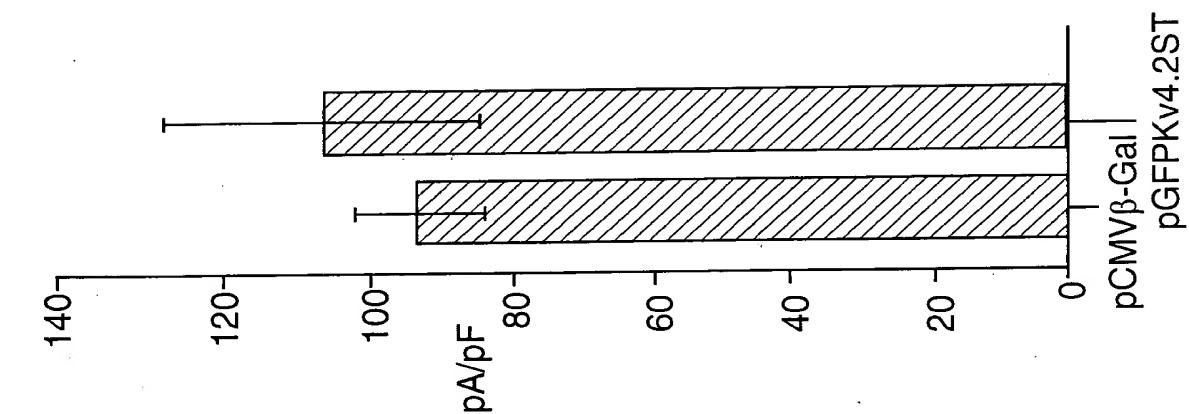


FIG. 14C

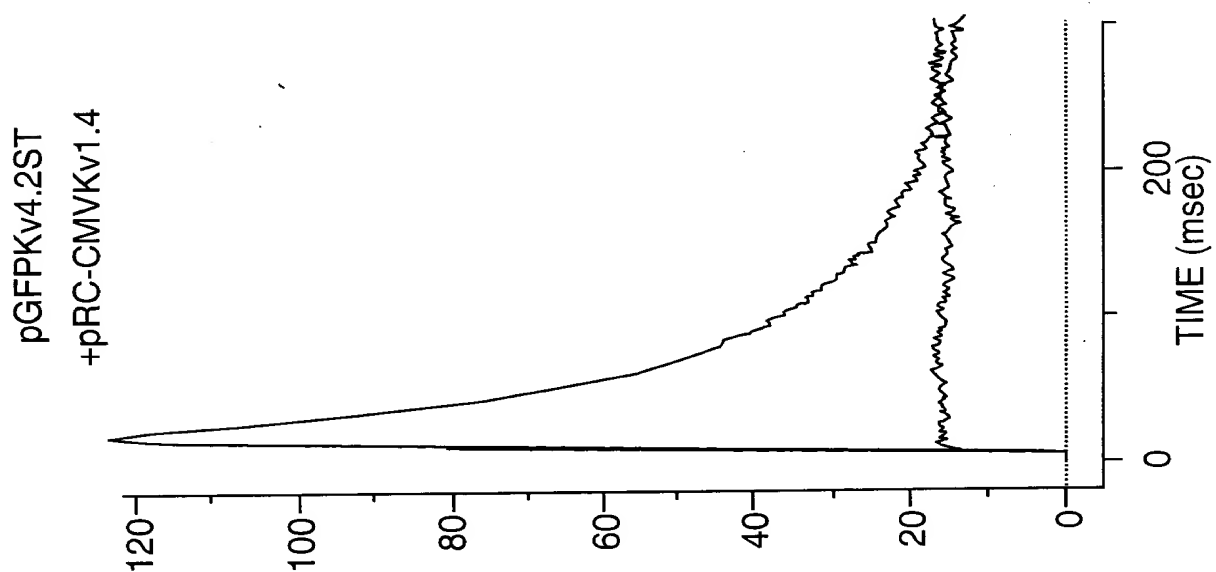


FIG. 14B

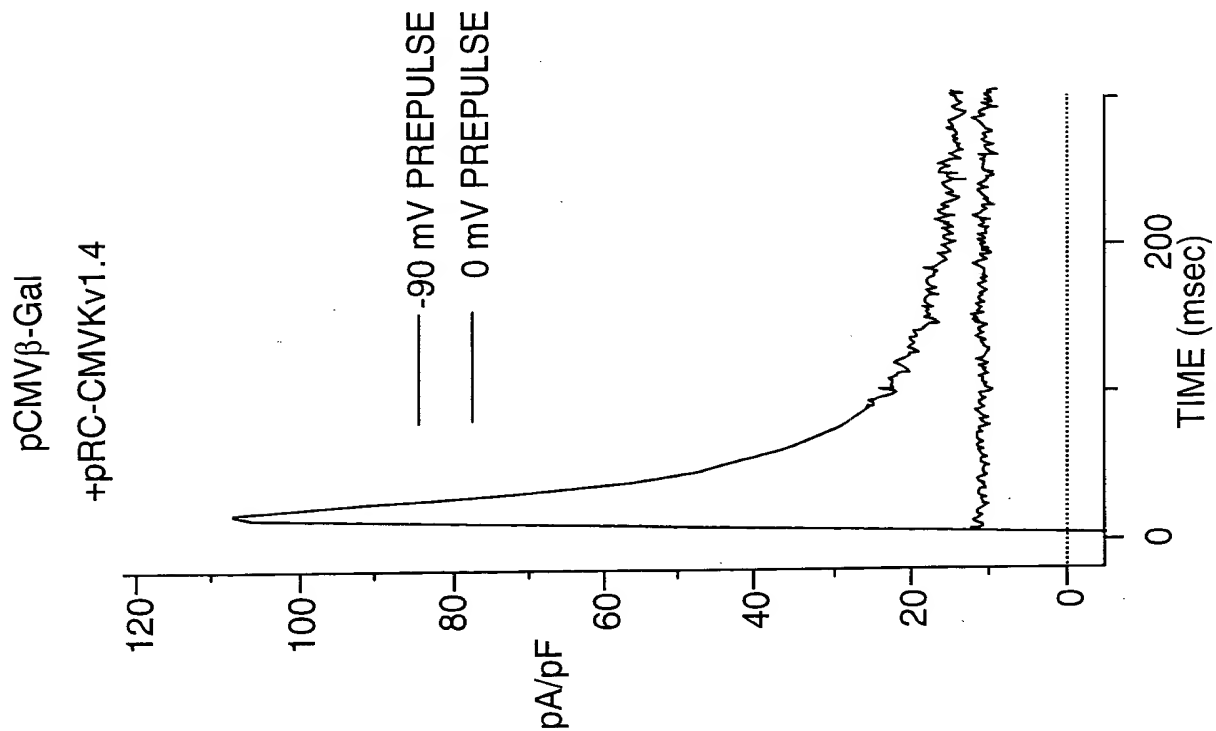


FIG. 14A

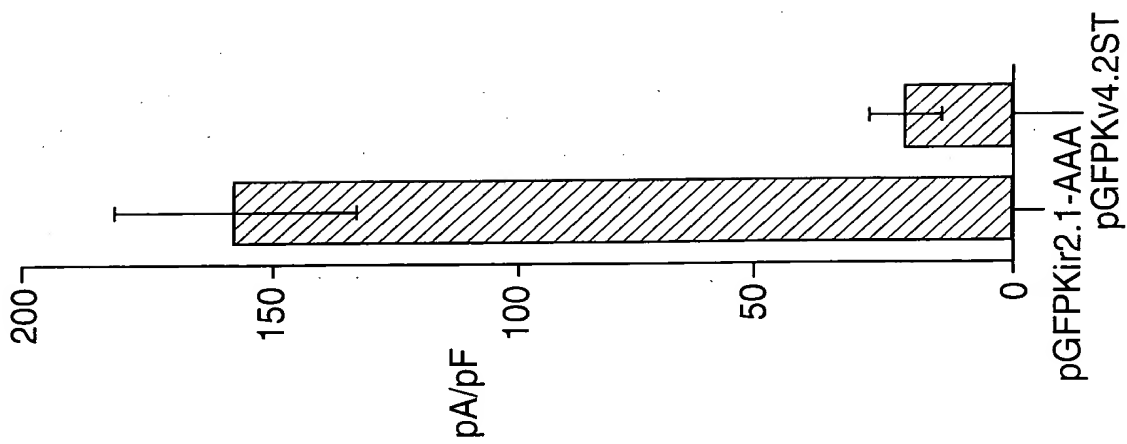


FIG. 14F

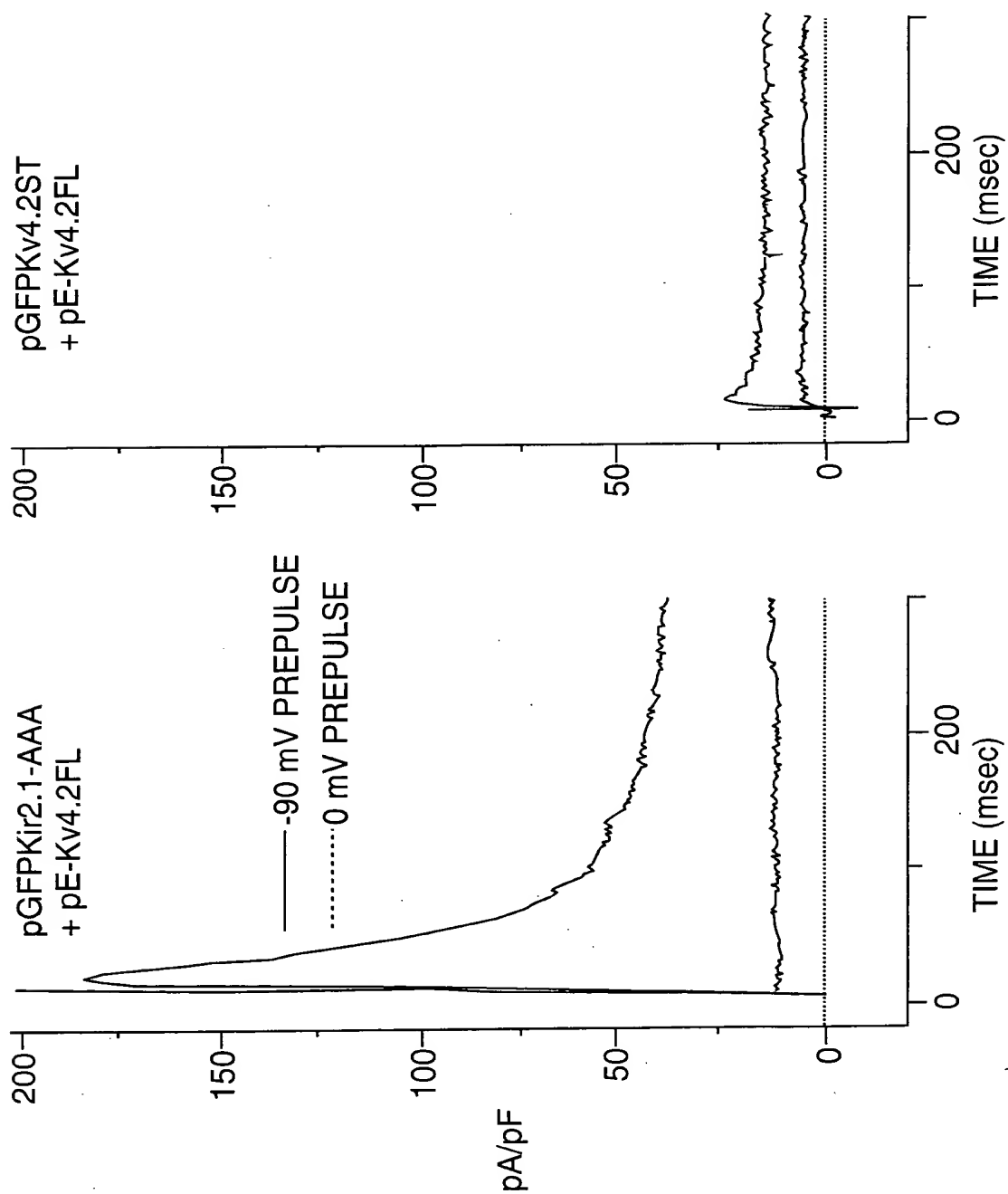


FIG. 14E

FIG. 14D

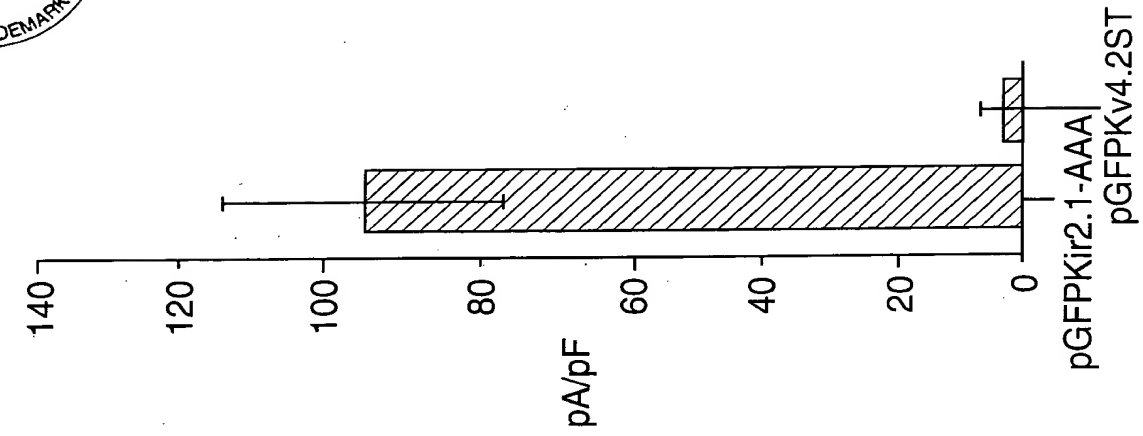


FIG. 14I

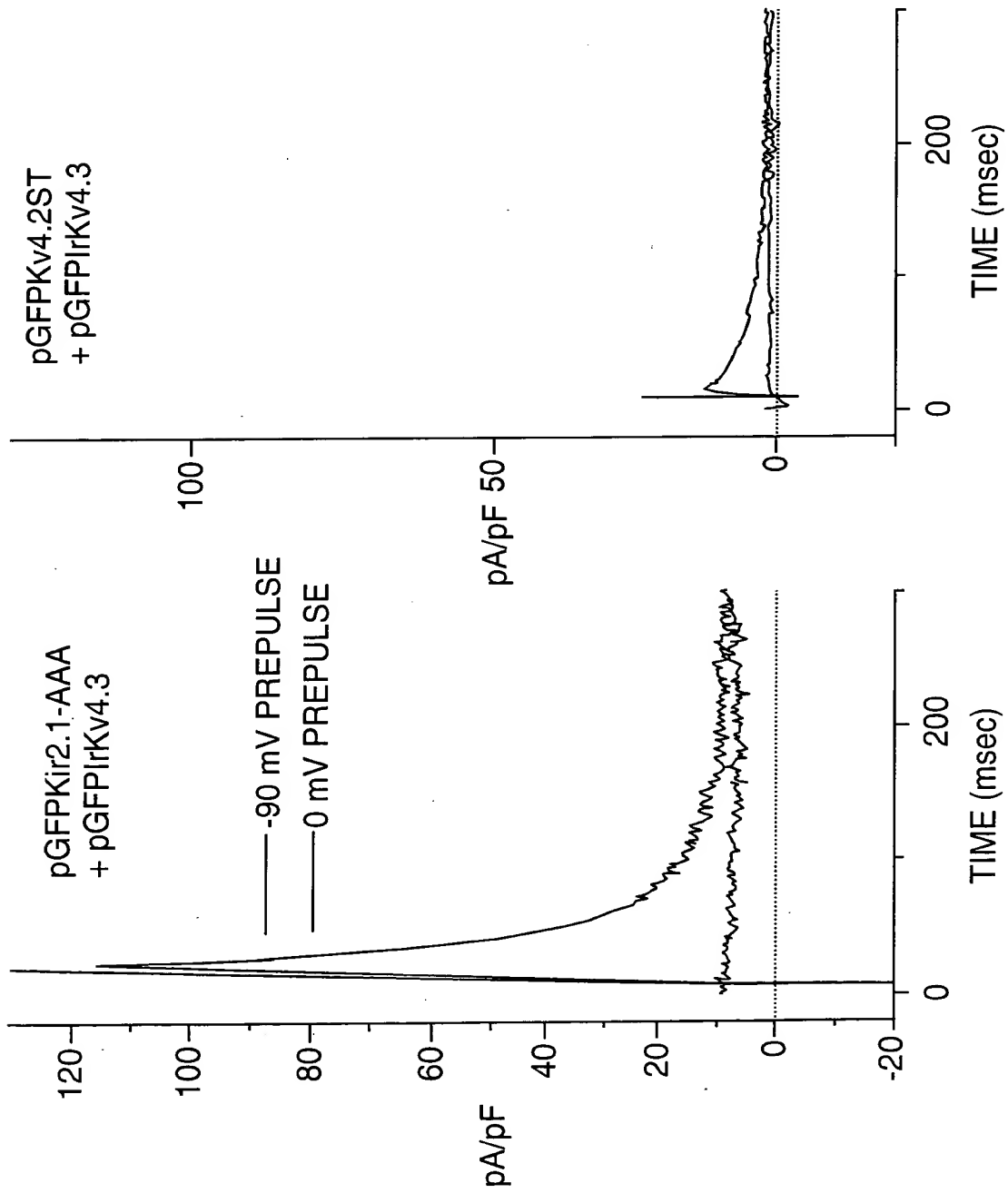


FIG. 14H

FIG. 14G



27/27



FIG. 15B



FIG. 15A

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